

SEQ SEARCH SUMMARY

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2003, 15:48:55 ; Search time 55475 Seconds
(without alignments)
11813.830 Million cell updates/sec

Title: US-09-830-160-1
Perfect score: 16020
Sequence: 1 agatctcgtccgccagtgcc.....caccggccgggagagatct 16020

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length	Match	Length			
c	1	15741.6	98.3	16065	1	AF187532	1	AF187532	Streptomy
c	2	1847	11.5	14807	1	AF264025	1	AF264025	Streptomy
c	3	1085.4	6.8	25883	1	AB008466	1	AB008466	Streptomy
c	4	882	5.5	9523	1	AF237894S1	1	AF237894	Streptomy
c	5	848.2	5.3	15052	1	AF055579	1	AF055579	Streptomy
	6	760.6	4.7	5084	1	SGSTRELMB	1	X62567	S.griseus s
c	7	689.8	4.3	18977	1	SAR7932	1	AJ007932	Streptomy
c	8	686.2	4.3	25459	1	SGAJ6985	1	AJ006985	Streptomy
c	9	665.4	4.2	2311	1	AF355468	1	AF355468	Saccharop
c	10	665.4	4.2	2363	6	AX089466	6	AX089466	Sequence
c	11	661.4	4.1	2310	6	AR165019	6	AR165019	Sequence
c	12	661.4	4.1	2310	6	AR281867	6	AR281867	Sequence
c	13	661.4	4.1	2310	6	BD137650	6	BD137650	Biosynthe
c	14	661.2	4.1	3500	1	SERORF1	1	L37354	Saccharopol
	15	656.6	4.1	4133	1	AB054887	1	AB054887	Streptomy
c	16	646.6	4.0	22999	1	AB088119	1	AB088119	Streptomy
c	17	636.6	4.0	56917	1	AME16952	1	Y16952	Amycolatops
c	18	607.8	3.8	37941	1	AOPCZA361	1	AJ223998	Amycolato
c	19	596	3.7	6085	6	A60304	6	A60304	Sequence 4
c	20	596	3.7	6085	6	AR144763	6	AR144763	Sequence
c	21	580.8	3.6	37116	6	AX574199	6	AX574199	Sequence
	22	580.8	3.6	109519	6	AX195929	6	AX195929	Sequence
c	23	579.8	3.6	2313	1	STMDNRI	1	M80237	S.peucetius
	24	579.6	3.6	38506	6	AR271680	6	AR271680	Sequence
	25	579.6	3.6	38506	6	AR277664	6	AR277664	Sequence
	26	578	3.6	12441	1	AF079762	1	AF079762	Streptomy.
c	27	577.8	3.6	1119	6	AX195932	6	AX195932	Sequence
c	28	577.8	3.6	1122	6	AX574132	6	AX574132	Sequence
c	29	577.8	3.6	1128	6	AX574130	6	AX574130	Sequence
c	30	577.8	3.6	10035	6	AX574202	6	AX574202	Sequence
c	31	577.8	3.6	11115	6	AX205014	6	AX205014	Sequence
c	32	577.8	3.6	47981	1	AF263245	1	AF263245	Micromono
c	33	577.8	3.6	47981	6	AX112026	6	AX112026	Sequence

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OM nucleic - nucleic search, using sw model

Run on: November 16, 2003, 15:48:55 ; Search time 3546 Seconds
(without alignments)
12195.431 Million cell updates/sec

Title: US-09-830-160-1
Perfect score: 16020
Sequence: 1 agatctcggtccgccagtgcc.....caccgcggccggagagatct 16020

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
- 6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
- 7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
- 8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
- 9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
- 10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
- 11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
- 12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
- 13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
- 16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
- 17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
- 18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
- 25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				DB	ID	Description
	No.	Score	Match	Length	Query	DB			
	1	15920	99.4	16020	21	AAA39283			Streptomyces nogal
c	2	1847	11.5	14806	22	AAD03809			Streptomyces galil
c	3	665.4	4.2	2363	22	AAF88340			S. spinosa polyket
c	4	661.4	4.1	2310	20	AAZ21502			Saccharopolyspora
c	5	596	3.7	6085	18	AAT70153			S.longisporoflavus
c	6	580.8	3.6	37116	25	ABZ66810			Orthosomycin biosy
	7	580.8	3.6	109519	22	AAS08693			Micromonospora DNA
	8	579.6	3.6	38506	21	AAA75633			Nucleotide sequenc
	9	579.6	3.6	38506	21	AAZ56001			Recombinant cosmid
	10	579.6	3.6	38506	25	ABS56090			S. venezuelae DNA
	11	578	3.6	12441	21	AAZ87284			S. venezuelae deso
	12	578	3.6	13613	24	AAD39043			Streptomyces venez
c	13	577.8	3.6	1122	25	ABZ66775			Orthosomycin biosy
c	14	577.8	3.6	1128	25	ABZ66774			Orthosomycin biosy
c	15	577.8	3.6	10035	25	ABZ66813			Orthosomycin biosy
c	16	577.8	3.6	11115	23	ABL50562			Micromonospora car
c	17	577.8	3.6	47981	22	AAF30757			Micromonospora meg
	18	561.6	3.5	1281	21	AAZ87292			S. venezuelae deso
	19	561.6	3.5	1281	24	AAD39050			Streptomyces venez
c	20	530.2	3.3	3412	20	AAX25772			S.erythraea erythr
	21	522.2	3.3	3756	18	AAT72684			Sugar biosynthesis
c	22	518.6	3.2	1600	24	AAS18441			Contig 88 DNA enco
c	23	516.2	3.2	42000	21	AAA63349			Streptomyces globi
c	24	516.2	3.2	63164	21	AAA63348			Streptomyces globi
	25	510.4	3.2	6093	20	AAX25775			S.erythraea oleand
	26	510.4	3.2	50937	21	AAA09469			Streptococcus olea
c	27	486.8	3.0	6854	19	AAT76903			S. glaucescens Pst
	28	485.6	3.0	1476	24	AAS18443			Contig 122 DNA enc
c	29	479.4	3.0	1266	20	AAX25773			S.erythraea erythr
c	30	475.2	3.0	3035	21	AAA63462			Streptomyces globi
c	31	474	3.0	3291	21	AAZ56004			Contig 003 from co
	32	473.6	3.0	14806	22	AAD03809			Streptomyces galil
c	33	472.4	2.9	3292	21	AAA75636			Nucleotide sequenc
c	34	472.4	2.9	3292	25	ABS56093			Contig 003 from co
	35	470.8	2.9	13613	21	AAZ87319			S. venezuelae deso
c	36	469.2	2.9	9994	22	AAC85191			S. avermitilis 10
	37	464.4	2.9	1272	20	AAZ21503			Saccharopolyspora
	38	464.2	2.9	19016	25	AAD47222			Streptococcus sp.
c	39	460.6	2.9	1014	21	AAZ87289			S. venezuelae deso
c	40	460.6	2.9	1014	24	AAD39047			Streptomyces venez
c	41	458.8	2.9	990	22	AAF88341			S. spinosa DNA fra
	42	452.8	2.8	9994	22	AAC85191			S. avermitilis 10
	43	437.4	2.7	47981	22	AAF30757			Micromonospora meg
	44	432.2	2.7	3291	21	AAZ56004			Contig 003 from co
	45	432.2	2.7	3292	21	AAA75636			Nucleotide sequenc

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: November 16, 2003, 15:52:15 ; Search time 754 Seconds
(without alignments)
9377.928 Million cell updates/sec

Title: US-09-830-160-1
Perfect score: 16020
Sequence: 1 agatctcgtccgccagtgcc.....caccgcggccggagagatct 16020

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%							
Result		Query							
No.	Score	Match	Length	DB	ID	Description			
c	1	661.4	4.1	2310	3	US-09-036-987A-25			Sequence 25, Appl
c	2	661.4	4.1	2310	3	US-09-370-700-25			Sequence 25, Appl
c	3	661.4	4.1	2310	4	US-09-603-207-25			Sequence 25, Appl
c	4	596	3.7	6085	3	US-09-029-603-4			Sequence 4, Appli
	5	579.6	3.6	38506	3	US-09-320-878-19			Sequence 19, Appl
	6	579.6	3.6	38506	4	US-09-141-908-1			Sequence 1, Appli
	7	579.6	3.6	38506	4	US-09-657-440-19			Sequence 19, Appl
	8	578	3.6	13613	3	US-09-105-537-3			Sequence 3, Appli
c	9	577.8	3.6	47981	4	US-09-679-279-1			Sequence 1, Appli
	10	561.6	3.5	1281	3	US-09-105-537-19			Sequence 19, Appl
	11	522.2	3.3	3756	2	US-08-576-626A-1			Sequence 1, Appli
c	12	518.6	3.2	1600	4	US-09-434-288-10			Sequence 10, Appl

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OM nucleic - nucleic search, using sw model

Run on: November 16, 2003, 15:52:15 ; Search time 4192 Seconds
(without alignments)
12489.655 Million cell updates/sec

Title: US-09-830-160-1
Perfect score: 16020
Sequence: 1 agatctcgtccgccagtgcc.....caccggccgggagagatct 16020
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2169961 seqs, 1634102185 residues
Total number of hits satisfying chosen parameters: 4339922

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	579.6	3.6	38506	11	US-09-793-708-19	Sequence 19, Appl
2	579.6	3.6	38506	12	US-10-201-365-1	Sequence 1, Appli
3	579.6	3.6	38506	12	US-10-160-539-19	Sequence 19, Appl
4	578	3.6	12441	11	US-09-988-384B-3	Sequence 3, Appli
5	578	3.6	13613	10	US-09-861-289-3	Sequence 3, Appli